

A note on the phases of natural evolution

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Abstract

The natural evolution of life seems to proceed through steps characterized by phases of relatively rapid changes, followed by longer, more stable periods. In the light of the string-theory derived physical scenario proposed in [1], we discuss how this behaviour can be related to a sequence of resonances of the energy of natural sources of radiation and absorption energies of the DNA, responsible for mutagenesis. In a scenario in which these energy scales run independently as functions of the age of the Universe, the conditions for evolutionary mutagenesis are satisfied only at discrete points of the time axis, and for a short period, corresponding to the width of the resonance. We consider in particular the evolution of the primates through subsequent steps of increasing cranio-facial contraction, and the great Eras of life (Paleozoic, Mesozoic, Cenozoic), showing that the transitions occur at the predicted times of resonance.

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Paleontological observations seem to indicate that the evolution of life would not take place “progressively”, but would be characterized by relatively short periods of “sudden” mutation, separated by longer, more or less “stable” periods. For instance, it has been observed that the species of hominids, from the primates to the homo sapiens, is characterized by an evolution toward an increasing cranio-facial contraction, which makes possible an expansion of the volume of the brain, and appears to take place at specific periods in which a big step forward is made, followed by longer periods in which this kind of mutagenesis seems to be “at rest” [2]. This progressing through “steps” seems in some way to call into question certain aspects of the (neo-)Darwinian theory of the evolution through natural selection. Why should not all the possible directions, i.e. all the possible mutations, be statistically generated at the same time? Why should then evolution not be a “continuum” process? This has even induced to talk about “ontogenesis” for this kind of mutations, and mathematical models have been investigated, in order to explain this behaviour [3, 4, 5].

We don’t want here to delve into the problematic of the “mechanics” of this progressive contraction. We are more generally interested in the biophysical dynamics of evolution, which seems to occur through a sequence of steps forward and rests, and this not only with regard to the human species, but also more in general to the big Eras of life on the Earth. In this note, we approach the problem from a point of view inspired by our recent work in fundamental physics, [1], where we consider the physics arising in the framework of a non-perturbative string theory scenario.

According to [1], all fundamental mass scales m_i , as well as the couplings of elementary particles α_j , are expected to mainly run, during the cosmological evolution, as appropriate roots of the (inverse) age of the Universe. Their dominant behaviour would therefore be of the type:

$$m_i \sim \frac{1}{\mathcal{T}^{\frac{1}{\gamma_i}}}, \quad \alpha_j \sim \frac{1}{\mathcal{T}^{\frac{1}{\gamma_j}}}, \quad \gamma_i, \gamma_j > 1, \quad (0.1)$$

where \mathcal{T} is the age of the Universe, measured in reduced Planck units (the units for which all the fundamental constants, namely the Planck constant \hbar , the speed of light c , and the Planck mass $1/\sqrt{G_N}$ are set to 1), and γ_i, γ_j are appropriate positive numbers, $\gamma_i, \gamma_j > 1$. As a consequence of 0.1, in first approximation also all atomic and molecular energy scales run, up to some normalization coefficients, as appropriate powers of the (inverse) age of the Universe:

$$E_p \sim \frac{1}{\mathcal{T}^{\frac{1}{p}}} + \mathcal{O}\left(\frac{1}{\mathcal{T}^{\frac{1}{q}}}\right), \quad p > q > 1. \quad (0.2)$$

Of course, in these units the age of the Universe is an adimensional quantity, it is a “pure number”, so that it must not surprise that an energy can correspond to any power of a time. In order to obtain something with the dimension of an energy, the r.h.s. of equation 0.2 must be eventually multiplied by the Planck mass times the speed of light to the square. At our present time, the rate of variation of couplings, masses, and energies, is very small, irrelevant for our experience of every day. However, it becomes significant as seen on a cosmological scale. But its effect is appreciable also at “intermediate” scales, such as those

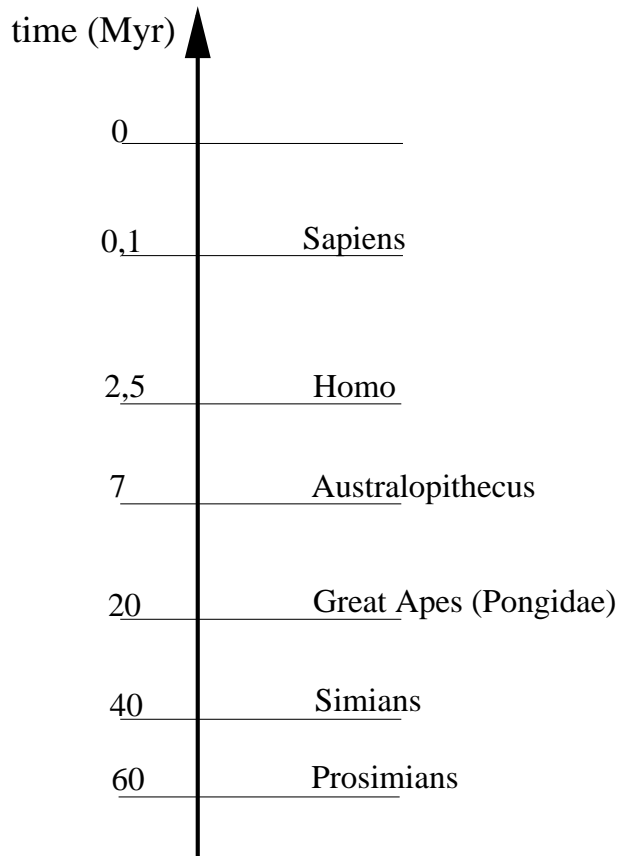


Figure 1: The steps of increasing cranio-facial contraction of hominids, according to [2].

of the evolution of life, where it can show out in “fine-tuning” effects. Among these are precisely the cases of natural evolution we are going to discuss.

Here we will discuss how the sequence of these evolutionary steps, as well as the relatively short duration of the intervals of “rapid” progress of the evolution, can be explained entirely within the laws of molecular physics and the Neo-Darwinian theory of natural evolution.

1 The evolution of Primates

Let’s consider first the example referring to the most recent series of evolutionary mutations: the evolution of primates along steps of increasing cranio-facial contraction, summarized in figure 1. It is clear that the duration of these periods increases as we go back in time to earlier ages, although no simple mathematical relation seems to relate them. Once expressed in units of the age of the Universe, the periods \mathcal{T}_n of the primates-to-human history show a behaviour much less unfamiliar. Indeed, as we will discuss, they approximately arrange into

a power series:

$$\mathcal{T}_n \approx k n^q, \quad (1.1)$$

for some positive numbers k and q , $0 < q < 1$, and n running on the natural numbers. What produces this behaviour? The fact that mutations seem to occur during a very short time, as compared to the duration of the “stable” phases, recalls the typical width of a resonance threshold in energy absorption processes. In a quantum system, energy levels are quantized and in general discrete; this is true at least as long as we consider a bound system and its binding energies, a situation to which the DNA corresponds with good approximation. Mutagenesis is a process produced by a change in the DNA structure. At the molecular level, what happens is that, as a consequence of the absorption of a certain amount of energy (e.g. radiation of a certain frequency), protons and/or electrons “jump” to different positions, and form new bonds. Let’s consider to expose the DNA to a certain kind of radiation. The energy that hits the probe is quantized, and is related to the frequency ν , or the wavelength λ , of the radiation, according to the Compton law:

$$E_{\text{source}} = h\nu = \frac{c}{\lambda}. \quad (1.2)$$

Also the energy levels of the target molecule are expected to be quantized. The typical energies of mutagenetic processes are the object of several investigations, based on approximations of the DNA sequence as a crystal, or in general a system bound in a certain region [6, 7, 8, 9]. In general, the absorption spectrum is discrete:

$$E_{DNA} = \{E(n)\}, \quad E(n) = k_n E_0, \quad (1.3)$$

where k_n is a certain coefficient and n runs on (a subset of) the natural numbers. The radiation energy 1.2 can be absorbed by the DNA molecule, and produce a change in its structure, only if it corresponds to one of the discrete levels of its spectrum. In this case, we have a resonance of the absorption probability:

$$E_{\text{source}}|_{\text{res.}} \cong E(n)_{\text{target}}. \quad (1.4)$$

A series of evolutionary steps, such as those of the progressive cranio-facial contraction, corresponds to a specific change of the DNA structure, possibly induced by a change of one or more proton bonds, that could be a transition of the kind considered in Ref. [6], or something similar. Which molecular bonds do correspond to a certain degree of contraction is not known. However, it is not unreasonable to think that the amount of contraction is related to the number of bonds which underwent an “elementary” transition in the DNA molecule. Let’s make the hypothesis that this is indeed the case. A larger degree of mutation would then correspond to a larger number of elementary transitions. In order to induce one such change, an “elementary step” A , the DNA molecule must absorb an energy:

$$E_A = E(n_A) = k_{n_A} E_0, \quad (1.5)$$

for some quantum number $n = n_A$. Let’s suppose that this is precisely induced by the absorption of energy coming from an external source of radiation. In order to induce the evolutionary mutation under consideration, we must therefore have:

$$E_{\text{source}}|_{\text{res.}} \cong E(n_A)_{\text{target}}. \quad (1.6)$$

A discrete series of resonance points along the time axis is only possible if the two energy scales run as independent functions of time. The amount of change at any such point should be related to the time width of the resonance.

As anticipated, let's suppose mutations are induced by radiation. There are several candidates for a source of radiation able to induce genetic mutations: the UV radiation, mostly coming from solar light; the natural radioactivity, and cosmic rays. However, X and cosmic rays are extremely energetic, and the mutations they induce are in general not “evolutionary” but “destructive”. The radiation that in practice can induce molecular changes leading to new forms of life, not just to the death of an organism, is the ultra-violet, and perhaps even less energetic, radiation. Therefore, the energy spectrum of the source should basically be the one of the electronic transitions, giving rise to the known atomic emission spectra (in the case of hydrogen, the Lyman series etc...).

During the cosmological evolution, the spectrum and the amount of this type of radiation have changed, according to the evolution of the stars and in particular of the solar system. However, for what matters our problem, restricted to a very recent era of the evolution of the Universe, it can be considered a sufficiently regular background ¹. Were the energy levels of the source, and of the target DNA, constant (as they are normally assumed to be), the mutation process would be progressive: the elementary transition would be constantly related to a certain spectral line, or a bunch of spectral lines. The rate of absorption would be proportional to the intensity of the source (almost constant), leading to a statistically continuous increase of the number of changed bonds in the DNA molecule. We would therefore observe a continuous evolution of primates. In the framework of the physical scenario discussed in Ref. [1], both the emitted radiation, and the ground energy scale of the DNA bonds, being functions of elementary energy scales and couplings, have a dominant behaviour given as in 0.2. This means that, in first approximation, they run as two independent powers of the age of the Universe:

$$E_{\text{source}} \approx \frac{k_s}{\mathcal{T}^{p_s}}; \quad (1.7)$$

$$E_{\text{target}} \approx \frac{k_t}{\mathcal{T}^{p_t}}, \quad (1.8)$$

where p_s, p_t are real numbers $0 < (p_s, p_t) < 1$, and k_s, k_t are coefficients that collect the contribution of symmetry factors and encode the dependence on the quantum numbers labelling the energy levels. At a generic time \mathcal{T} , the radiated energy doesn't correspond to any energy gap of the target. Let's suppose that at a certain age \mathcal{T}_i we have a resonance with some spectral line of the source:

$$E(n_A) \approx E_{\text{source}}(n, m), \quad (1.9)$$

¹We refer here to the frequencies of the spectrum, and in general the cosmological running of the fundamental physical parameters. We don't consider variations due, for instance, to the solar activity, that don't affect such properties. We will comment about these effects in section 3.

where (n, m) is a shorthand notation that indicates the quantum numbers of the two energy levels involved in the transition producing the radiation in the source. When 1.9 is satisfied, energy can be absorbed, making possible for the system to undergo a class of genetic mutations, corresponding to new possible DNA molecular changes. Statistically, in a short time, corresponding to the width of the resonance, all possible mutations are tried out. There is therefore not necessarily a unique kind of mutation. The maximal transition probability is attained at the pick of the resonance. Out of this point, the probability rapidly decays, at a speed depending on the characteristic width of emission and absorption spectra. In any case, after a “short” time, these transitions are no more possible (i.e. they are extremely suppressed), and the rate of the mutagenesis process drops down dramatically. Natural selection will then decide which one(s) among all the mutations will survive. The system will then “stabilize” until a new resonance threshold opens up. Suppose this was a facial bone contraction enabling a larger brain volume; we get a certain amount of contraction-inducing transitions (i.e. a certain amount of changed DNA bonds), depending on the width of the resonance window. Then the process stops till the new resonance. This occurs when the same kind of molecular transitions are induced by the next spectral line that turns out to meet the condition 1.9. If a larger brain is a mutation favoured by natural selection also at later times, then, at the next resonance time, Nature will favour again the same kind of transition; the suspended process of contraction will be resumed and progress for another while, leading to the birth of species of primates with a still larger brain.

We can give a rough estimate of the separation between subsequent resonance times. First of all, let’s see what is the order of magnitude we should expect for the exponents p_s and p_t of eqs. 1.7 and 1.8. For the emission scale, under the hypothesis of an atomic origin of the radiation, whatever is the source of radiation in first approximation the atomic energy levels are given as some numbers multiplied by the Rydberg constant R . This is strictly true only in the simplest case, the hydrogen atom, in which case the energy levels are given by:

$$E_{\text{source}}(n, m) = h\nu = R \left(\frac{1}{m^2} - \frac{1}{n^2} \right), \quad (1.10)$$

where:

$$R \approx R_\infty = m_e \alpha^2 / 4\pi \quad (\times c/\hbar), \quad (1.11)$$

where m_e is the electron’s mass and α the fine structure constant (in our framework, neither of them is constant). The highest energy, ultra-violet series, is obtained with $m = 1$ (Lyman series). More in general, the energy levels have more complicated expressions, and, for heavy elements, with many electrons, one has to consider also relativistic effects scaling as $m_e \alpha^4$. However, as long as we are interested in a rough estimate, we will assume here that the energy levels of our source have an effective approximate hydrogen-like spectrum. This hypothesis is on the other hand supported by the consideration that hydrogen is the most common element in the Universe. We expect therefore that the energy levels behave approximately as the Lyman series:

$$E_{\text{source}} \approx R_\infty \left(1 - \frac{1}{n^2} \right). \quad (1.12)$$

For the target DNA molecule, the energy levels of interest for us are those corresponding to a transition not among the positions of the electrons but of the protons (see for instance

Ref. [6, 10]). We don't know what is the dominant term in the typical energy scale of mutagenetic transitions; therefore, here we leave open the possibility that the fundamental, time-dependent part of the binding energies could even be more sensitive to the proton (and neutron) mass, than to the electron's mass. Even in the lack of a precise knowledge about the details of the DNA energies, let's suppose that their fundamental scale is different from the one of the source of radiation. In this case, there are two possibilities:

- 1) The DNA fundamental scale runs slower, and therefore is above, the scale of the source. In this case, since $1/m^2 - 1/n^2 < 1$, a resonance of the source with the target, 1.9, is only possible if:

$$k_{n_A} < 1, \quad (1.13)$$

with k_{n_A} as defined in 1.5. This could be the case if we think that, having to deal with energy levels related to bound states of protons, instead than of electrons, for what concerns the transitions of interest for us, the fundamental DNA energy scale $E_0 = E_0^{\text{target}}$, defined in 1.5, roughly has a dominant behaviour analogous to the one of the atomic scale, 1.11, but with the proton mass instead than the electron's mass. Namely, it could be something like $E_0^{\text{target}} \approx m_p \alpha^2$.

- 2) The DNA fundamental scale runs faster, and therefore is below, the scale of the source. This can be the case if the dependence on the coupling α is realized through a higher power, something that would reduce the scale to lie below the scale 1.11, by "eating" the gain due to a higher proton mass, or simply by suppressing by a higher amount the electron's mass scale, so that:

$$E_0^{\text{target}} \approx m_{(p/e)} \alpha^\beta < E_{\text{source}}, \quad \beta > 2, \quad (1.14)$$

and

$$k_{n_A} > 1. \quad (1.15)$$

According to [1], both the electron mass and the electric charge (the fine structure constant α) run as positive roots of the inverse of the age of the Universe. This means that the Rydberg constant too scales as a certain root of the age of the Universe. At sufficiently large times as compared to the Planck length (as is the case of the evolution of life), also the proton mass roughly scales as a root of the age of the Universe. With reference to equations 1.7 and 1.8, we can therefore identify:

$$\frac{1}{\mathcal{T}^{p_s}} \sim R_\infty = R_\infty(\mathcal{T}) \equiv E_{\text{source}}^0(\mathcal{T}); \quad (1.16)$$

$$\frac{1}{\mathcal{T}^{p_t}} \sim E_{\text{target}}^0(\mathcal{T}). \quad (1.17)$$

For the purpose of the present discussion, there is no fundamental difference between case (1) or (2). Important for our argument is just that we assume that the DNA ground energy scale runs with time differently from the scale of the source. However, the choice of the one or the other of (1) and (2) implies a deep difference in the interpretation when we consider larger time scales, as we will comment at the end of the analysis. If we suppose here that

the DNA fundamental scale runs slower than (and therefore is above) the atomic scale of the source, case (1), then:

$$p_s > p_t . \quad (1.18)$$

If instead we suppose that the DNA fundamental scale runs faster than (and therefore is below) the atomic scale of the source, case (2), we have:

$$p_s < p_t . \quad (1.19)$$

In both cases, the resonance condition 1.9 at a time \mathcal{T}_i can be written as:

$$\mathcal{T}_i^{p_s - p_t} \approx k_{n_A} \times \left(1 - \frac{1}{n_i^2} \right) . \quad (1.20)$$

In case (1) the series of \mathcal{T}_i progresses toward higher n (higher energy levels of the source); in case (2) the series of \mathcal{T}_i progresses toward lower n (lower energy levels of the source).

We can work out what is the sequence of times between such resonances, namely, the differences:

$$\mathcal{T}_{i+1} - \mathcal{T}_i, \quad \mathcal{T}_{i+2} - \mathcal{T}_{i+1}, \quad \dots , \quad (1.21)$$

by solving the equation 1.20 for $n_i = n$, $n_{i+1} = n+1$, $n_{i+2} = n+2, \dots$ if $p_s > p_t$ (case 1), and for $n_i = n$, $n_{i+1} = n-1$, $n_{i+2} = n-2, \dots$ if $p_s < p_t$ (case 2). Let's introduce $q \equiv 1/(p_t - p_s)$. Clearly, $|q| > 1$; we can then write equation 1.20 as:

$$\mathcal{T}_i \approx \left[k_{n_A} \times \left(1 - \frac{1}{n_i^2} \right) \right]^q , \quad (1.22)$$

where the choice of sign of the exponent, $\pm |q|$, depends on whether the physical situation corresponds to case 1) or 2).

In order to verify our hypothesis, we fit equation 1.22 over five points in the history of the Universe, corresponding to the turning periods in which mutagenesis has produced the evolution of the human species from the Australopithecus to the Homo Sapiens, illustrated in figure 1 of page 2. A first problem of such a numerical computation is that the age of the Universe is only known with a rough approximation. The common estimates range from 11,4 to 15 billion years. As we discussed in Ref. [1], this value could be an over-estimate: within the framework of [1] everything seems to be consistent with a slightly shorter age, of around 9,6 billion years. To be "conservative", we will assume an age of the Universe of around 10 billion years. After all, we are here interested in just a rough estimate: other, perhaps larger, inaccuracies could affect our calculation. A major problem of this interpolation is however that the age of the universe, measured in reduced Planck units, whatever its value precisely is, is an extremely huge number: $\sim \mathcal{O}(10^{60})$. Generic curve-fitting algorithms are not able to deal with such numbers, and try to find the best interpolation by reducing the parameters to numbers of order 1. In order to get rid of big numbers and constant parameters, we plot therefore the quantity:

$$y(x) \equiv \frac{\mathcal{T}_{\ell+x}}{\mathcal{T}_\ell} , \quad (1.23)$$

for the five values from “Simians” to “Sapiens” as given in figure 1². From expression 1.22 we obtain:

$$\frac{\mathcal{T}_{i+N}}{\mathcal{T}_i} \cong \left[\frac{1 - \frac{1}{(n_i + (\text{sgn } q)N)^2}}{1 - \frac{1}{n_i^2}} \right]^q. \quad (1.24)$$

For mass and energy scales ranging at present time from the meV to the keV scale, the exponents p_s and p_t have typical values in the range $\sim [\frac{1}{2} - \frac{1}{2.4}]$. Therefore, $|q| \gg 1$. Limiting the analysis to the first values of N , namely $N = 1, 2, 3, 4, 5$, we can assume that $N \ll n_i$. Under these conditions, expression 1.24 can be approximated by:

$$y(N) \sim N^c, \quad N = 1, 2, 3 \dots \quad (1.25)$$

for some constant c . The small spacing of the periods, $\mathcal{T}_{i+1} - \mathcal{T}_i$, as compared to the age of the Universe, tells us that $c \ll 1$. This approximation is valid as long as we can write:

$$N \approx \left[\frac{1 - \frac{1}{(n + (\text{sgn } q)\tilde{N})^2}}{1 - \frac{1}{n^2}} \right]^{\frac{q}{c}}, \quad \tilde{N} \equiv \pm(N - 1), \quad (1.26)$$

where we have shifted the value of N on the r.h.s. to $\tilde{N} = (N - 1)$ in order to account for the fact that the point $N = 1$ of the interpolation corresponds to the point $\tilde{N} = 0$ on the r.h.s. Notice that, while the sequence of numbers on the l.h.s. increases over the natural numbers, on the r.h.s. the sequence runs over the integers. Namely, in the case the exponent $q < -1$, the progression is toward decreasing energy levels of the source. This is obvious, because in this case as time goes by the DNA scale becomes smaller and smaller as compared to the scale of the source, and the resonance is realized with lower energies of the source. For n sufficiently large, $n > |\tilde{N}|$, we can expand the r.h.s. of 1.26 as:

$$\left[\frac{1 - \frac{1}{(n + \tilde{N})^2}}{1 - \frac{1}{n^2}} \right]^{\frac{q}{c}} \approx \left[1 \pm \frac{2|\tilde{N}|}{n^3} + \mathcal{O} \left(\frac{1}{n^2} \times \left(\frac{\tilde{N}}{n} \right)^2 \right) \dots \right]^{\pm \frac{|q|}{c}}. \quad (1.27)$$

By keeping just the first two terms of the expansion, we have a binomial raised to the power q/c , and we obtain:

$$N \approx 1 + \left(\frac{q}{c} \right) \frac{2\tilde{N}}{n^3} + \dots, \quad (1.28)$$

where the neglected terms receive a contribution from what we neglected in 1.27, of order:

$$\sim \mathcal{O} \left[\left(\frac{\tilde{N}}{n^2} \right)^2 \right]; \quad (1.29)$$

and from the higher order terms in the binomial expansion:

$$\sim \mathcal{O} \left[\left(\frac{2\tilde{N}}{n^3} \right)^2 \right]. \quad (1.30)$$

²We exclude the edge value corresponding to the prosimians, on which we will comment later.

The term $(q/c)2\tilde{N}/n^3$ in eq. 1.28 is always positive, because either is $q > 0$, with an increasing sequence of numbers in the atomic source, $\tilde{N} > 0$, or is $q < 0$, and the matching condition is realized through a series of decreasing energies of the source, $\tilde{N} < 0$. In either case, equation 1.28 is approximately solved by:

$$n \sim \left(\frac{2|q|}{c} \right)^{1/3}. \quad (1.31)$$

Notice that this kind of approximation may work also for atomic sequences other than the Lyman series. For a generic $1/m$ in expression 1.10 we would obtain an expression analogous to 1.28, simply with rescaled quantities: $n \rightarrow n/m$, $\tilde{N} \rightarrow \tilde{N}/m$, resulting in a solution:

$$n \sim \left(\frac{2m^2|q|}{c} \right)^{1/3}. \quad (1.32)$$

Therefore, we don't really need to assume that the energies of the source correspond to the Lyman series. For what we have just discussed, it is reasonable to fit the ratios 1.24, referred to the five last steps of the evolution of primates, with the curve:

$$y = a x^c. \quad (1.33)$$

Assuming an age of the universe of $\sim 10^{10}$ yr, the values \mathcal{T}_i can be approximated as:

$$\begin{aligned} \mathcal{T}_1 &\approx 1,002 \times 10^{10} \text{ yr}; \\ \mathcal{T}_2 &\approx 1,004 \times 10^{10} \text{ yr}; \\ \mathcal{T}_3 &\approx 1,0053 \times 10^{10} \text{ yr}; \\ \mathcal{T}_4 &\approx 1,00575 \times 10^{10} \text{ yr}; \\ \mathcal{T}_5 &\approx 1,00599 \times 10^{10} \text{ yr}. \end{aligned} \quad (1.34)$$

By testing several interpolation options, we have seen that it doesn't make a big difference to fit the curve 1.33 or to allow for a shift of the x value, namely the curve:

$$y = a(x - b)^c. \quad (1.35)$$

In any case, the computer solves the problem by finding a very small exponent c , and a parameter a of order 1. The results are plotted in figures 3 and 4. The curve fitting gives in the case 1.33:

$$\begin{aligned} a &= 1.0001526590176328; \\ c &= 2.5513644365246610 \times 10^{-3}, \end{aligned} \quad (1.36)$$

and, in the case of a shifted power, 1.35:

$$\begin{aligned} a &= 1.0015925425865762; \\ b &= 3.8904855104367164 \times 10^{-1}; \\ c &= 1.6992267577200736 \times 10^{-3}. \end{aligned} \quad (1.37)$$

We have tested the interpolation in several ways, and seen that there can be a certain variation of these parameters, according to the interpolation algorithm, and the preferences set for the interpolation. Their values are therefore only roughly indicative. Within this approximation, the fit is also not so sensitive to a slight variation of the value of the age of the Universe.

1.1 The step of Prosimians

At large n , the atomic energy levels get closer and closer to each other (the atomic series converge to specific frequencies at the limit $n \rightarrow \infty$). In the case (2) a larger atomic quantum number n is found at earlier times. In this case, by going toward the early steps of the sequence of resonances, the emitted energies accumulate to a “continuum”, which could appear as a wider width of a unique resonance³. Moreover, in this regime the time intervals become approximately equal. The condition:

$$\mathcal{T}_{n+1} - \mathcal{T}_{n+1} \approx \mathcal{T}_{n+2} - \mathcal{T}_{n+1}, \quad (1.38)$$

is in fact approximately equivalent to:

$$\left(1 - \frac{1}{(n+1)^2}\right)^p - \left(1 - \frac{1}{n^2}\right)^p \approx \left(1 - \frac{1}{(n+2)^2}\right)^p - \left(1 - \frac{1}{(n+1)^2}\right)^p, \quad (1.39)$$

which is verified up to orders $\mathcal{O}\left[\frac{1}{(n+1)^2}\right]$. For lower quantum numbers, the approximation 1.26 neglects smaller terms (1.29, 1.30), but as we approach a larger quantum number, also the terms neglected in the “linear” approximation 1.38 are small enough. It could be that the starting point of the “prosimians” period in figure 1, page 2, apparently falling out of the sequence, precisely lies at the transition between the two kinds of approximations we are making. Moreover, we can expect that early times are estimated with a lower accuracy. Does this time lie at the border of the series, so that earlier resonances simply “accumulate” within the time width of a unique resonance, in such a way that this appears as the first, “large” resonance time of this kind of mutation?

In the scenario (1), at earlier times the resonance is realized with lower energy levels of the source. In principle, at very earlier times, the mutation could be induced by other atomic series, lower than the Lyman one. Indeed, this series corresponds to the ultraviolet light only at present time, and according to the scenario (1) at earlier ages of the Universe its energies were higher as compared with those of the DNA bonds. In this case, it could be that the step corresponding to the beginning of prosimians corresponds to a value of n at which our approximation, valid for n sufficiently large, starts to fail, and perhaps corresponds to the end of a lower series. However, a rough numerical check doesn’t speak in favour of this hypothesis. If also the beginning of the prosimians era has to be accounted within this series of evolutionary steps, then the scenario (2) seems to be favoured. In this case, as \mathcal{T} increases,

³This even though the ratio of the fundamental scales, i.e. the one of the source and the one of the DNA bonds under consideration, undergoes an accelerated increase as time goes by, and therefore the time intervals become shorter.

more kinds of molecular transitions become possible, in correspondence to higher molecular levels becoming accessible to a resonance with the highest atomic series. On the other hand, the time windows allowed for a mutation become narrower and narrower, because the scale $1/T^{p_s-p_t}$ becomes smaller. Owing to the smaller time width, in the average a smaller number of elementary transitions occur during a resonance. As a consequence, it becomes also smaller the average increase of the cranio-facial contraction. We should therefore expect that the evolution of the species tends to “smooth down” toward more frequent but less dramatic changes.

2 The great Eras of life: the Paleozoic, Mesozoic and Cenozoic steps

The coincidence with a DNA absorption resonance should in principle be at the ground of evolutionary processes that don't refer only to the primates: it should work for any form of life. A problem is to identify which sets of mutations can be grouped into classes corresponding to the same “basic” transition, and therefore can be arranged along the same series of neighbouring resonances. It is not hard to imagine that the evolutionary processes can be distinguished into several classes, according to the kind of molecular transitions they are controlled by. For instance, by looking at figure 2, one can figure out that the big subdivision into Paleozoic, Mesozoic and Cenozoic Eras of the natural evolution should not mix with the “sub-eras”, the Periods such as the Triassic, the Jurassic etc..., although these periods not necessarily fit into subclasses of the main class of transition. This means that not necessarily “Triassic, Jurassic and Cretaceous” belong to the same main class, distinguished from the class formed by the set “Cambrian, Ordovician, Silurian, Devonian, Carboniferous, Permian”. The beginning of the first era, the Paleozoic Era, is the time when most of the major groups of animals first appear in the fossil record, and is sometimes called the “Cambrian Explosion”, because of the relatively short time over which this diversity of forms appeared. The Triassic-Permian extinction event too is something that took place in a relative short interval of time. Lastly, the end of the Mesozoic era is characterized by the sudden disappearance of dinosaurs. These facts strongly suggest that also the beginning and the end of these eras were marked by a rapid evolution, as due to the opening of new resonance thresholds allowing genetic mutation. We may ask whether also these big eras of the evolution of life follow a power-law sequence.

Taking as “resonance points” the ages corresponding to the beginning of the Paleozoic era, the transition to the Mesozoic, and from Mesozoic to Cenozoic, we obtain the following sequence:

$$\begin{aligned} \mathcal{T}'_1 &\approx 1,0000 \times 10^{10} \text{ yr} ; \\ \mathcal{T}'_2 &\approx 1,0350 \times 10^{10} \text{ yr} ; \\ \mathcal{T}'_3 &\approx 1,0535 \times 10^{10} \text{ yr} , \end{aligned} \tag{2.1}$$

where, for the sake of simplicity, we have rounded the basic time, at the starting point of the Paleozoic era, to 10 billion years. Actually, in figure 2 there is a fourth age, our present time. However, although, as discussed above, it seems that we are at turning point of a new mutation process, this corresponds to a series of resonance energies that, for what we

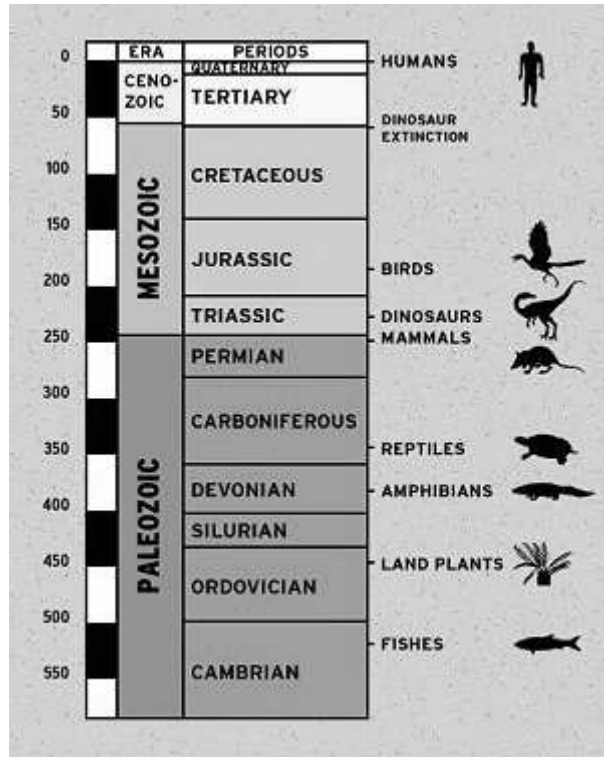


Figure 2: The great Eras of the evolution of life.

have seen, it is safe to consider distinguished from the one we are considering now: it starts later, being entirely included within the Cenozoic era. If the ages 2.1 are going to belong to a sequence of resonances, this is quite probably another series, which reaches the first resonance well before. All this to say that from our interpolation we exclude our present time, that would correspond to:

$$\mathcal{T}'_4 \approx 1,0600 \times 10^{10} \text{ yr} . \quad (2.2)$$

By proceeding in the same way as in section 1, we plot the values $y(x)$. Unfortunately, we have only three data for our interpolation. Nevertheless, the agreement of these data with the fitting curve, as it can be seen from the diagrams 5 and 6, is remarkable. The coefficient of the curve 1.33 are now:

$$\begin{aligned} a' &= 1.0003919688516729 ; \\ c' &= 4.7632362251061745 \times 10^{-2} , \end{aligned} \quad (2.3)$$

and, for the curve 1.35,

$$\begin{aligned} a' &= 1,0150031204496974 ; \\ b' &= -3,2534837743317041 \times 10^{-1} ; \\ c' &= 3,7838527455527071E \times 10^{-2} , \end{aligned} \quad (2.4)$$

where the b' coefficient comes with a negative sign because, for computational reasons, we shifted the first x value from 0 to 1. Once shifted back, the correct b coefficient is:

$$\bar{b}' = 1 - b' = 0,67465162256682959 . \quad (2.5)$$

As we already observed, the values of the interpolation coefficients are only approximately indicative. A really significant output is on the other hand the fact that the coefficients c' differ from the c of section 1 by one order of magnitude. This value is higher than the statistical uncertainty due to the artifacts of the interpolation algorithm. The difference between the two coefficients is therefore something real, and signals that we are in the presence of absorption resonances corresponding to a different series and power law. This on the other hand is precisely what we should expect, on the base of the consideration that the genetic mutations are of another kind. In this case, they could correspond to different DNA transition energies. Indeed, the power-law behaviour 1.25 is basically due to the power-law scaling of the ratio of the basic scales $E_{\text{source}}^0/E_{\text{target}}^0$, and the fact that within a certain range the quantum energy levels can be approximated by a simple harmonic oscillator-like expression $E(n) \approx nE_0$. A quantum system in a box approximately correspond to a three-dimensional harmonic oscillator. In the case of DNA, we can suppose that it roughly corresponds to a composite system of many harmonic oscillators. In this way, at the first order the coefficient k_n in 1.3 should be given by:

$$k_n \approx (n + n_0)k_0 , \quad (2.6)$$

where k_0 is a scaling factor and n_0 is the ground energy, a quantum Casimir effect that, if in the case of a one-dimensional harmonic oscillator is $1/2$, in a complex system consisting

of many harmonic oscillators can be a much larger number. If this is the case, then, keeping fixed the quantum numbers of the energy of the source, a power-law sequence 1.25 is obtained as long as we can approximate:

$$\left(\frac{n + \tilde{N} + n_0}{n + n_0}\right)^{\frac{q}{c}} \approx 1 + \left(\frac{q}{c}\right) \frac{\tilde{N}}{n + n_0} + \mathcal{O}\left(\frac{\tilde{N}}{n + n_0}\right)^2, \quad (2.7)$$

by retaining only the first two terms, and identifying this time:

$$\frac{q}{c} \sim n + n_0, \quad (2.8)$$

for some n . This is certainly possible, if the ground number n_0 is sufficiently large. In practice, the fact of having a sequence of the type 1.25 is related to the possibility of making a linear approximation of the spacing of the energy levels, either of the source or of the target, or both of them, into steps of equal separation, at fixed fundamental energy scale. Once the running of the latter is taken into account, this translates into a series of the type 1.1.

Under these hypotheses, our analysis tells us that also the three big eras of the evolution, the Paleozoic, Mesozoic and Cenozoic, fit in a series of resonances. According to these results, we may ask whether the disappearance of dinosaurs, the event that marks the end of the Mesozoic era, could be ascribed to the appearance of more evolved competitors, perhaps coming from a mutation of already existing species. It appears in fact the more and more clear that their extinction, although it surely took place in a time interval very short as compared to the length of their period of existence, it has been a process much longer than what we would have expected if it was produced by some “external” catastrophic event, and perhaps better suits to a typical resonance width. We know that eventually mammals prevailed, although they already existed well before; could it be that a slight mutation finally gave them the necessary advantage to prevail over dinosaurs?

Plugging the coefficients 2.3 or 2.4 in equation 1.33 (or 1.35 respectively), we can also speculate about when should the Cenozoic era have an end. Solving 1.33 for $x = 4$ we obtain that this should correspond to a time \mathcal{T}_4 such that:

$$\frac{\mathcal{T}_4}{\mathcal{T}_1} \approx 1,069, \quad (2.9)$$

and, in the case of the curve 1.35:

$$\frac{\mathcal{T}_4}{\mathcal{T}_1} \approx 1,073. \quad (2.10)$$

This means in around 9 million years, or 13 in the case of the shifted-power curve 1.35. These predictions should be taken with a pinch of salt: 9, or 13 millions years, is a huge number as compared to the human history, but a little one if compared to the length of the Paleozoic and Mesozoic eras: a difference of a dozen of millions in the estimate of the length of the Cenozoic era would reflect in an error of just a few percents in the estimate of the curve. For instance, had we included in the interpolation also our present time, given in 2.2, as the end point of an era, we would have obtained the following fits:

$$\begin{aligned} a'' &= 1.0020109359413651; \\ c'' &= 4.3037554472469014 \times 10^{-2}. \end{aligned} \quad (2.11)$$

and

$$\begin{aligned} a'' &= 1.0277362232536369; \\ b'' &= -6,4503233764454060 \times 10^{-1}; \\ c'' &= 2.6484826008431502 \times 10^{-2}. \end{aligned} \tag{2.12}$$

The plots are illustrated in figures 7 and 8 , and show that still the fits would be acceptable. With these coefficients, the end point of the era starting at our present time, would be estimated to have its end in some 14 (resp. 15) millions years.

3 Remarks

At this point, several considerations are in order:

- Two different classes of the evolution, namely the one of the big eras of life on the earth, and the one of the primates, seem to arrange into sequences corresponding to DNA resonance energies. What distinguishes these two classes? For what we have seen, different series could be characterized by:

1. A different ratio k_s/k_t , where k_s and k_t are given in eqs. 1.7 and 1.8. This means that the fundamental energy scales of both the source of radiation and the DNA are the same, but the mutations are produced by transitions corresponding to different energy levels of the same kind of source of radiation, and/or different energy levels in the DNA bonds;
2. A differently running fundamental energy scale, either in the source (eq. 1.16), or in the target DNA (eq. 1.17), or in both of them. Since the time dependence of these scales is a consequence of the time dependence of the electron's mass and charge, a different time scaling could be the consequence of a different dependence of the energy levels on these quantities, as well as on other time-dependent parameters, such as the proton mass. This could be the case of mutations produced by another class of DNA transitions.

Our approximation, and the small number of experimental data, together with their relative inaccuracy, don't allow us to see finer differentiations and discriminate between slightly different descriptions of the molecular and atomic physics. A more accurate analysis of the natural evolution could indeed provide some insight in the structure of these energy levels, and open new perspectives to the investigation of the DNA, providing more insight into its structure and the dynamics of mutagenesis. A small example of the possibilities offered by this method is given by our discussion of the scenarios (1) and (2) of the evolution of the primates. In that case, a conclusion in favour of one of the two possibilities (namely, the scenario 2) gives non trivial information about the DNA energy scales.

At our present state of knowledge, we cannot decide out of any doubt what distinguishes the sequence of the human evolution from the larger evolutionary scale of the three main eras of figure 2. In the case of the evolution of primates, we assumed that *the same* kind of

molecular transition acts at any time there is a resonance condition. The amount of progress in the evolution, according to [2] proportional to the amount of cranio-facial contraction, would then be proportional to the number of occurred molecular transitions in the DNA. A priori it is not clear whether also in the case of the sequence of the big eras of figure 2, a unique kind of mutation is at work during all the turning periods. Intuitively, we would say that in this case it is not, and the fact that the interpolation of these periods with the power-law curve, figures 5 and 6, gives an even better fit than in the case of Primates, seems to be rather in favour of the interpretation that in this case the different turning times correspond to different energy levels of the DNA, because in this case the spacing is expected to be more regular. The question remains however open; the seek for an answer could lead to a deeper understanding of the mechanisms of DNA transitions and their relation to the evolution.

- Obviously, different molecular transitions lead to different mutations. Therefore, the entire history of the evolution cannot fit into a single series. However, in general not necessarily all the steps of the evolution can be ordered into some series. A simple look at eras, ages and periods, shows that there are many “irregular” periods, which apparently cannot be arranged into any ordered sequence. Indeed, there can be a huge variety of combinations of DNA and source energy levels, leading to different mutations. Owing to the superposition of different mutations and different periods, the history of the evolution may not look so easily well ordered. It remains however a key point that these transitions occur at “discrete” points of the time axis, a feature that naturally fits with our scenario of time-running energy scales.

- The time spread of a mutation period does not depend only on the width of a resonance, but also on the fact that natural radiation is not “coherent”, it has a certain spread of frequencies.

- The main source of UV radiation coming to the earth is the sun. Its activity is not constant; however, the solar phases involve the amount of produced radiation, not its being in resonance or not. As a consequence, under the hypothesis that the major cause of evolutionary mutagenesis is the solar light, what we expect is that variations of the solar activity affect the evolution process only if they fall within the time window of some resonance; in this case the mutation process can be accelerated (or slowed down).

- For simplicity, we did not consider mutagenesis of plants. In principle, these too could (should?) follow similar laws, and perhaps the full story about evolution of species is the result of an interaction/interference of all these phenomena.

All these considerations make only sense within the scenario proposed in [1], in which the energy scales depend on time. Only in this case we obtain a discrete sequence of “resonance” periods. Otherwise, the full spectrum of emission from natural sources, as well as the complete spectrum of molecular energy levels, would be fixed and constant all along the history. The conditions for a genetic mutation would then be always the same, and mutations would be statistically generated without interruption. A step-wise progress of the evolution would then require completely different explanations.

We stress that, when expressed in terms of the time separating these periods from our present time, as in figures 1 and 2, the power-law scaling, relation 1.1, is not explicit. The situation is similar to the one of the law of a perfect gas, $PV = nRT$, in which the proportionality between pressure/volume and the temperature is only unveiled when the latter is expressed in terms of the absolute Kelvin scale. Analogously, here in order to see the relation we must express the time periods in terms of the absolute age of the Universe.

Despite the caution one must have in considering curve fitting, and the large inaccuracy of data, made more dramatic by the small number of points among which to interpolate, it remains a remarkable fact that, if expressed in terms of the astronomical, “absolute” time scale, the main periods of the evolution of life seem to arrange into series of steps corresponding to resonance thresholds of typical molecular and atomic energy series. This is by no means underestimating the role possibly played by other factors, which may act as “disturbing” agents, such as deep climatic changes due to solar phases, meteorites, supernova-neutrino effects and so on. And certainly, in the history of life many “sub-periods” seem to follow a more irregular path. But certainly, it is intriguing to see that, perhaps, the main steps are something “regular” and absolutely “programmed”. Not by something external to the rules of natural evolution and selection; simply, something intrinsic of the fundamental laws of physics.

According to the scenario discussed in Ref. [1], the Universe is expected to evolve toward more entropic configurations, in which the minimal energy step, which is also the size of the “unit cell” of the phase space, decreases. This agrees with the fact that the duration of the various phases decreases, making the more and more frequent the transition points. It however also means that the changes, the mutations, which are to be expected, should become less dramatic: more frequent, but also in the average smaller, steps.

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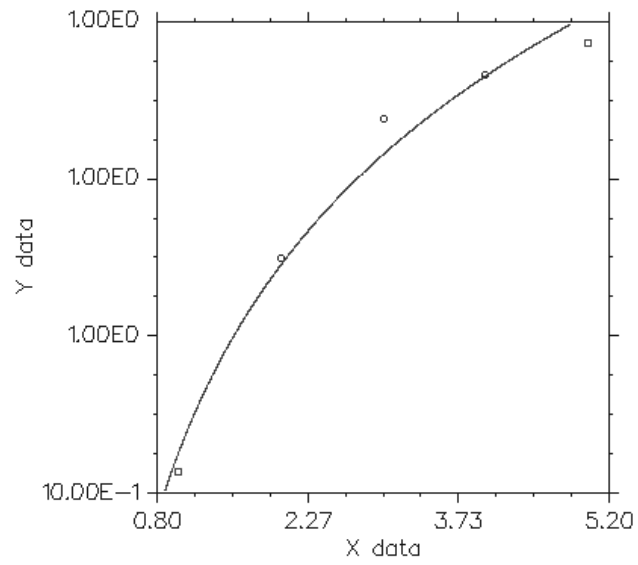


Figure 3: interpolation of human evolution with the curve $y = ax^c$.

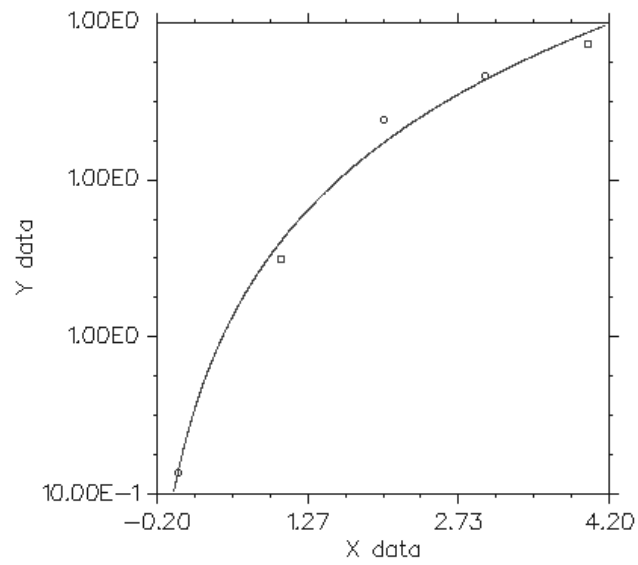


Figure 4: interpolation of human evolution with the curve $y = a(x - b)^c$.

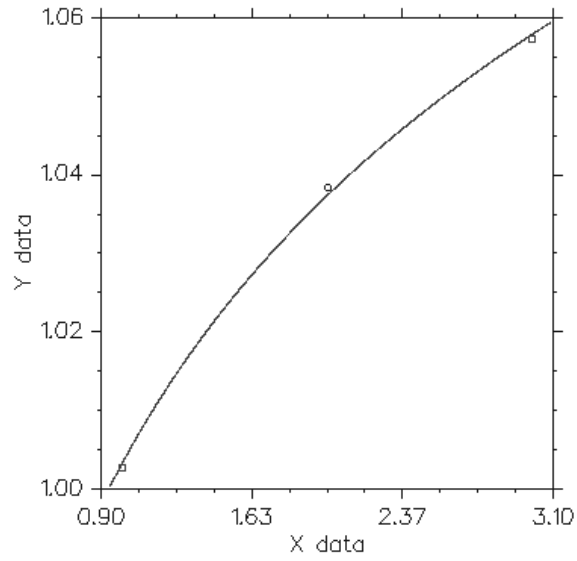


Figure 5: interpolation of the duration of the eras of figure 2 with the curve $y = ax^c$ (3 values).

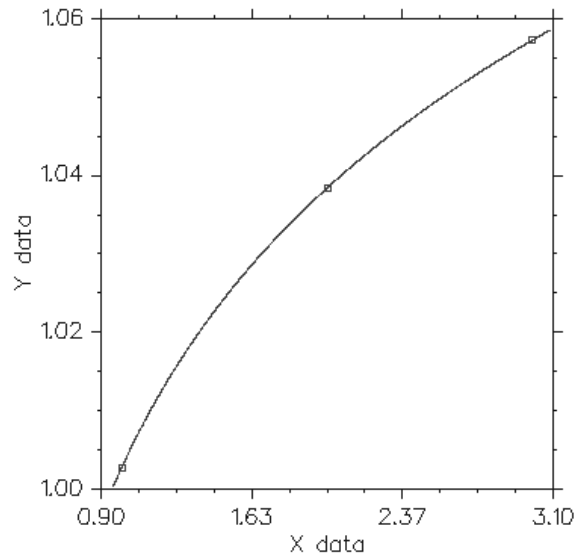


Figure 6: interpolation of the eras of figure 2 with the curve $y = a(x-b)^c$ (3 values). Notice that here, for computational reasons, we shifted the first x value from 0 to 1

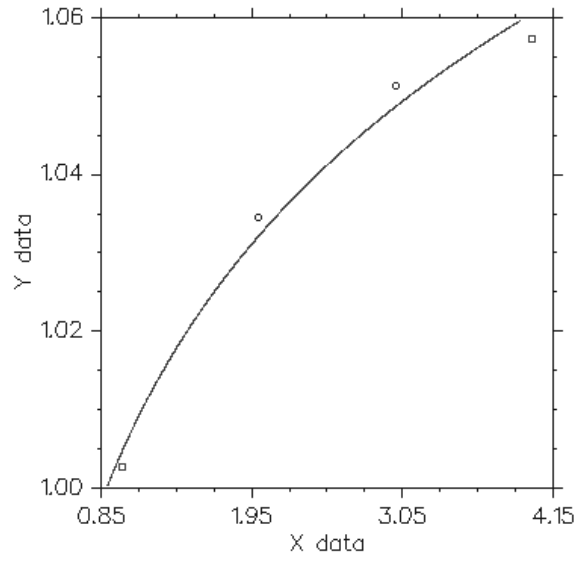


Figure 7: interpolation of the eras of figure 2 with the curve $y = ax^c$ (4 values).

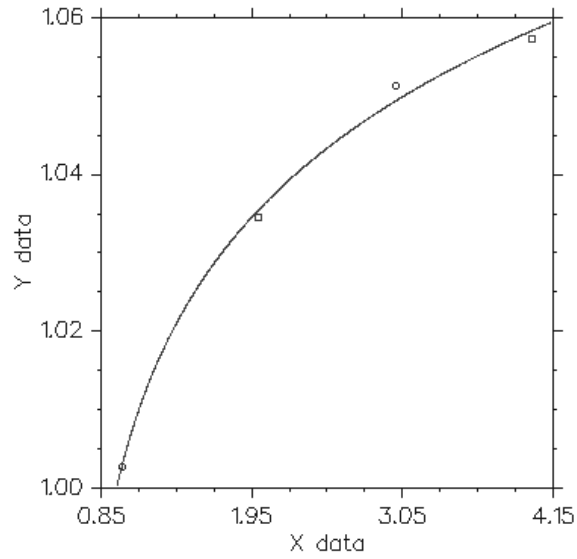


Figure 8: interpolation of the eras of figure 2 with the curve $y = a(x - b)^c$ (4 values).